SEQUENCE LISTING

(1) GENERAL INFORMATION:

10100

- (i) APPLICANT: Caras, Ingrid W
- (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 10
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/635130
 - (B) FILING DATE: 19-Mar-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Torchia, PhD., Timothy E.
 - (B) REGISTRATION NUMBER: 36,700
 - (C) REFERENCE/DOCKET NUMBER: P1001
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-8674
 - (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1877 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear



(ix) FEATURE:

- (A) NAME/KEY: Extra Cellular Domain
- (B) LOCATION: 244-899
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Transmembrane Domain
- (B) LOCATION: 901-978
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: signal peptide
- (B) LOCATION: 244-321
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GNTCTAGAAN TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCT 50

GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100

CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150

CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200

TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTC ATG 246

Met

1

GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
5 10

GCC CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
Ala Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
15 20 25

CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363 Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys 30 35 40

AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402 Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln 45

ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441 Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg 60 CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480 Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr 70 75 AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519 Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558 Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp 95 100 105 CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597 Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln 110 115 GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636 Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser 120 125 130 CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675 His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr 135 140 CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714 Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu 145 150 155 ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753 Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser 160 165 170 CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792 Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu 175 180 ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831 Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu 185 190 195 GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870 Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser



205

			GGT Gly 215				CCT Pro	909
			GTG Val				CTG Leu 235	948
			GGC Gly				GCC Ala	987
			CGG Arg					1026
			GGC Gly					1065
			GGA Gly 280					1104
			CTA Leu					1143
			CCC Pro					1182
			GGG Gly					1221
			AGC Ser					1260
			GAG Glu 345					1299
			CGA Arg					1338



ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
370 375

TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416 Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro 380 385 390

TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455 Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg 395 400

ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG 1494 Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr 405 410 415

GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT GGG AGG 1533

Ala Leu Phe Val Leu Val Leu Ile Leu Leu Gly Arg
420
430

CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572 Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala 435 440

AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610 Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu 445 450 455

ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660
GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710
CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA 1760
TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810
CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTCGA TATCAAGCTT 1860
ATCGATACCG TCGACCT 1877

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:



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Met 1	Gly	Pro	Pro	His 5	Ser	Gly	Pro	Gly	Gly 10	Val	Arg	Val	Gly	Ala 15
Leu	Leu	Leu	Leu	Gly 20	Val	Leu	Gly	Leu	Val 25	Ser	Gly	Leu	Ser	Leu 30
Glu	Pro	Val	Tyr	Trp 35	Asn	Ser	Ala	Asn	Lys 40	Arg	Phe	Gln	Ala	Glu 45
Gly	Gly	Tyr	Val	Leu 50	Tyr	Pro	Gln	Ile	Gly 55	Asp	Arg	Leu	Asp	Leu 60
Leu	Cys	Pro	Arg	Ala 65	Arg	Pro	Pro	Gly	Pro 70	His	Ser	Ser	Pro	Asn 75
¬ Tyr	Glu	Phe	Tyr	Lys 80	Leu	Tyr	Leu	Val	Gly 85	Gly	Ala	Gln	Gly	Arg 90
Arg	Cys	Glu	Ala	Pro 95	Pro	Ala	Pro	Asn	Leu 100	Leu	Leu	Thr	Cys	Asp 105
Arg	Pro	Asp	Leu	Asp 110	Leu	Arg	Phe	Thr	Ile 115	Lys	Phe	Gln	Glu	Tyr 120
Ser	Pro	Asn	Leu	Trp 125	Gly	His	Glu	Phe	Arg 130	Ser	His	His	Asp	Tyr 135
Tyr	Ile	Ile	Ala	Thr 140	Ser	Asp	Gly	Thr	Arg 145	Glu	Gly	Leu	Glu	Ser 150
Leu	Gln	Gly	Gly	Val 155	Cys	Leu	Thr	Arg	Gly 160	Met	Lys	Val	Leu	Leu 165
Arg	Val	Gly	Gln	Ser 170	Pro	Arg	Gly	Gly	Ala 175	Val	Pro	Arg	Lys	Pro 180
Val	Ser	Glu	Met	Pro 185	Met	Glu	Arg	Asp	Arg 190	Gly	Ala	Ala	His	Ser 195
Leu	Glu	Pro	Gly	Lys 200	Glu	Asn	Leu	Pro	Gly 205	Asp	Pro	Thr	Ser	Asn 210
Ala	Thr	Ser	Arg	Gly 215	Ala	Glu	Gly	Pro	Leu 220	Pro	Pro	Pro	Ser	Met 225
Pro	Ala	Val	Ala	Gly 230	Ala	Ala	Gly	Gly	Leu 235	Ala	Leu	Leu	Leu	Leu 240





Glv	Va 1	Ala	Glv	Ala	Gly	Glv	Δla	Met	Cvs	Trn	Ara	Ara	Ara	Ara
011	var	1114	011	245	Cry	Cly	1114	1100	250	112	1119	111.9	111.9	255
Ala	Lys	Pro	Ser	Glu 260	Ser	Arg	His	Pro	Gly 265	Pro	Gly	Ser	Phe	Gly 270
Arg	Gly	Gly	Ser	Leu 275	Gly	Leu	Gly	Gly	Gly 280	Gly	Gly	Met	Gly	Pro 285
Arg	Glu	Ala	Glu	Pro 290	Gly	Glu	Leu	Gly	Ile 295	Ala	Leu	Arg	Gly	Gly 300
Gly	Ala	Ala	Asp	Pro 305	Pro	Phe	Cys	Pro	His 310	Tyr	Glu	Lys	Val	Ser 315
Gly	Asp	Tyr	Gly	His 320	Pro	Val	Tyr	Ile	Val 325	Gln	Asp	Gly	Pro	Pro 330
Gln	Ser	Pro	Pro	Asn 335	Ile	Tyr	Tyr	Thr	Ser 340	Ile	Ser	Val	Leu	Glu 345
Trp	Pro	Ile	Leu	His 350	Thr	Ile	Gln	Leu	Phe 355	Phe	Met	Arg	Ser	Lys 360
Cys	Ser	Arg	Val	Thr 365	Thr	Phe	Leu	Phe	Pro 370	Val	Gln	Val	Ile	Thr 375
Thr	Ser	Thr	Cys	Arg 380	Met	Thr	Ser	Phe	Ser 385	Phe	Thr	Thr	Leu	Asn 390
Pro	Ser	Met	Gln	Ala 395	Cys	Arg	Ala	Gln	Met 400	Gly	Glu	Phe	Arg	Ile 405
Arg	Trp	Cys	Phe	Trp 410	Gly	Asp	Arg	Ile	Leu 415	Gly	Thr	Ala	Leu	Phe 420
Val	Leu	Val	Leu	Ile 425	Leu	Leu	Leu	Gly	Arg 430	Leu	Asn	Met	His	Gln 435
Thr	Thr	Leu	Leu	Arg 440	Gln	Arg	Ala	Ser	Val 445	Glu	Ala	Glu	Ala	Gly 450
Gln	His	Gly	Pro	Leu 455										

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100 CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200 TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTCATGGGGC 250 CCCCCCATTC TGGGCCGGGG GGCGTGCGAG TCGGGGCCCT GCTGCTGCTG 300 GGGGTTTTGG GGCTGGTGTC TGGGCTCAGC CTGGAGCCTG TCTACTGGAA 350 CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCTC 400 AGATCGGGGA CCGCTAGAC CTGCTCTGCC CCCGGGCCCG GCCTCCTGGC 450 CCTCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGG 500 TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA 550 CTTGTGATCG CCCAGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAG 600 TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA 650 CATCATTGCC ACATCGGATG GGACCCGGGA GGGCCTGGAG AGCCTGCAGG 700 GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA 750 AGTCCCGAG GAGGGGCTGT CCCCGAAAA CCTGTGTCTG AAATGCCCAT 800 GGAAAGAGAC CGAGGGGCAG CCCACAGCCT GGAGCCTGGG AAGGAGAACC 850 TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC 900 CTGCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGC 950 GCTGCTCTTG CTGGGCGTGG CAGGGGCTGG GGGTGCCATG TGTTGGCGGA 1000

GNTCTAGAAN TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCT 50





GACGGCGGGC	CAAGCCTTCG	GAGAGTCGCC	ACCCTGGTCC	TGGCTCCTTC	1050
GGGAGGGGAG	GGTCTCTGGG	CCTGGGGGGT	GGAGGTGGGA	TGGGACCTCG	1100
GGAGGCTGAG	CCTGGGGAGC	TAGGGATAGC	TCTGCGGGGT	GGCGGGGCTG	1150
CAGATCCCCC	CTTCTGCCCC	CACTATGAGA	AGGTGAGTGG	TGACTATGGG	1200
CATCCTGTGT	ATATCGTGCA	GGATGGGCCC	CCCCAGAGCC	CTCCAAACAT	1250
CTACTACAAG	GTATGAGGGC	TCCTCTCACG	TGGCTATCCT	GAATCCAGCC	1300
CTTCTTGGGG	TGCTCCTCCA	GTTTAATTCC	TGGTTTGAGG	GACACCTCTA	1350
ACATCTCGGC	CCCCTGTGCC	CCCCCAGCCC	CTTCACTCCT	CCCGGCTGCT	1400
GTCCTCGTCT	CCACTTTTAG	GATTCCTTAG	GATTCCCACT	GCCCCACTTC	1450
CTGCCCTCCC	GTTTGGCCAT	GGGTGCCCCC	CTCTGTCTCA	GTGTCCCTGG	1500
ATCCTTTTTC	CTTGGGGAGG	GGCACAGGCT	CAGCCTCCTC	TCTGACCATG	1550
ACCCAGGCAT	CCTTGTCCCC	CTCACCCACC	CAGAGCTAGG	GGCGGGAACA	1600
GCCCACCTTT	TGGTTGGCAC	CGCCTTCTTT	CTGCCTCTCA	CTGGTTTTCT	1650
CTTCTCTATC	TCTTATTCTT	TCCCTCTCTT	CCGTCTCTAG	GTCTGTTCTT	1700
CTTCCCTAGC	ATCCTCCTCC	CCACATCTCC	TTTCACCCTC	TTGGCTTCTT	1750
ATCCTGTGCC	TCTCCCATCT	CCTGGGTGGG	GGCATCAAAG	CATTTCTCCC	1800
CTTAGCTTTC	AGCCCCCTT	CTGACCTCTC	ATACCAACCA	CTCCCTCAG	1850
TCTGCCAAAA	ATGGGGGCCT	TATGGGGAAG	GCTCTGACAC	TCCACCCCAG	1900
CTCAGGCCAT	GGGCAGCAGG	GCTCCATTCT	CTGGCCTGGC	CCAGGCCTCT	1950
ACATACTTAC	TCCAGCCATT	TGGGGTGGTT	GGGTCATGAC	AGCTACCATG	2000
AGAAGAAGTG	TCCCGTTTTG	TCCAGTGGCC	AATAGCAAGA	TATGAACCGG	2050
TCGGGACATG	TATGGACTTG	GTCTGATGCT	GAATGGGCCA	CTTGGGACCG	2100
GAAGTGACTT	GCTCCAGACA	AGAGGTGACC	AGGCCCGGAC	AGAAATGGCC	2150
TGGGAAGTAG	CAGAAGCAGT	GCAGCAGGAA	CTGGAAGTGC	CTTCATCCAG	2200







GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACTCCAA 2250
GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300
GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACTT 2350
ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu 50 55 60

Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn 65 70 75

Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg 80 85 90

Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp 95 100 105

Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln Glu Tyr 110 115 120

Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser His His Asp Tyr 125 130 135

Tyr Ile Ile Ala Thr Ser Asp Gly Thr Arg Glu Gly Leu Glu Ser 140 145 150



Lêu	Gln	Gly	Gly	Val 155	Cys	Leu	Thr	Arg	Gly 160	Met	Lys	Val	Leu	Leu 165
Arg	Val	Gly	Gln	Ser 170	Pro	Arg	Gly	Gly	Ala 175	Val	Pro	Arg	Lys	Pro 180
Val	Ser	Glu	Met	Pro 185	Met	Glu	Arg	Asp	Arg 190	Gly	Ala	Ala	His	Ser 195
Leu	Glu	Pro	Gly	Lys 200	Glu	Asn	Leu	Pro	Gly 205	Asp	Pro	Thr	Ser	Asn 210
Ala	Thr	Ser	Arg	Gly 215	Ala	Glu	Gly	Pro	Leu 220	Pro	Pro	Pro	Ser	Met 225
Pro	Ala	Val	Ala	Gly 230	Ala	Ala	Gly	Gly	Leu 235	Ala	Leu	Leu	Leu	Leu 240
Gly	Val	Ala	Gly	Ala 245	Gly	Gly	Ala	Met	Cys 250	Trp	Arg	Arg	Arg	Arg 255
Ala	Lys	Pro	Ser	Glu 260	Ser	Arg	His	Pro	Gly 265	Pro	Gly	Ser	Phe	Gly 270
Arg	Gly	Gly	Ser	Leu 275	Gly	Leu	Gly	Gly	Gly 280	Gly	Gly	Met	Gly	Pro 285
Arg	Glu	Ala	Glu	Pro 290	Gly	Ğlu	Leu	Gly	Ile 295	Ala	Leu	Arg	Gly	Gly 300
Gly	Ala	Ala	Asp	Pro 305	Pro	Phe	Cys	Pro	His 310	Tyr	Glu	Lys	Val	Ser 315
Gly	Asp	Tyr	Gly	His 320	Pro	Val	Tyr	Ile	Val 325	Gln	Asp	Gly	Pro	Pro 330
Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Lys	Val					

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs

335

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:





GCCGACGCTG TGAGGCACCC CCTGCCCCAA ACCTCCTTCT CACTTGTGAT 50
CGCCCAGACC TGGATCTCCG CTTCACCATC AAGTTCCAGG AGTATAGCCC 100
TAATCTCTGG GGCCACGAGT TCCGCTCGCA CCACGATTAC TACATCATTG 150
CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAGTGTG 200
TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNGGAC AAAGTCCCGA 250
GGAGGGGCTG TCCCCCGAAA ACCTGTGTCT GAAATGCCCA TGGAAAGAGA 300
CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAGGAGA ACCTGCCAGG 350
TGACCCCACC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA 400
CCCTTTCCCA GCATTGCNTG CANTTGGTTN GGGGCAGCAN GGGGGNGTTT 450
TGGC 454



(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro 1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50
CCCATGGAAA 60





(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCCC CTCGGTCTCT 50
TTCCATGGGC 60

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala 1 5 10 15

Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys
20 25 30

Asn Leu Glu Pro Val Ser Trp Ser Ser Leu Asn Pro Lys Phe Leu 35 40 45

Ser Gly Lys Gly Leu Val Ile Tyr Pro Lys Ile Gly Asp Lys Leu 50 55 60

Asp Ile Ile Cys Pro Arg Ala Glu Ala Gly Arg Pro Tyr Glu Tyr
65 70 75

Tyr Lys Leu Tyr Leu Val Arg Pro Glu Gln Ala Ala Cys Ser 80 85 90

Thr Val Leu Asp Pro Asn Val Leu Val Thr Cys Asn Arg Pro Glu 95 100 105

Gln Glu Ile Arg Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro Asn 110 115 120

Tÿr	Met	Gly	Leu	Glu 125	Phe	Lys	Lys	His	His 130	Asp	Tyr	Tyr	Ile	Thr 135
Ser	Thr	Ser	Asn	Gly 140	Ser	Leu	Glu	Gly	Leu 145	Glu	Asn	Arg	Glu	Gly 150
Gly	Val	Cys	Arg	Thr 155	Arg	Thr	Met	Lys	Ile 160	Ile	Met	Lys	Val	Gly 165
Gln	Asp	Pro	Asn	Ala 170	Val	Thr	Pro	Glu	Gln 175	Leu	Thr	Thr	Ser	Arg 180
Pro	Ser	Lys	Glu	Ala 185	Asp	Asn	Thr	Val	Lys 190	Met	Ala	Thr	Gln	Ala 195
Pro	Gly	Ser	Arg	Gly 200	Ser	Leu	Gly	Asp	Ser 205	Asp	Gly	Lys	His	Glu 210
Thr	Val	Asn	Gln	Glu 215	Glu	Lys	Ser	Gly	Pro 220	Gly	Ala	Ser	Gly	Gly 225
Ser	Ser	Gly	Asp	Pro 230	Asp	Gly	Phe	Phe	Asn 235	Ser	Lys	Val	Ala	Leu 240
Phe	Ala	Ala	Val	Gly 245	Ala	Gly	Cys	Val	Ile 250	Phe	Leu	Leu	Ile	Ile 255
Ile	Phe	Leu	Thr	Val 260	Leu	Leu	Leu	Lys	Leu 265	Arg	Lys	Arg	His	Arg 270
Lys	His	Thr	Gln	Gln 275	Arg	Ala	Ala	Ala	Leu 280	Ser	Leu	Ser	Thr	Leu 285
Ala	Ser	Pro	Lys	Gly 290	Gly	Ser	Gly	Thr	Ala 295	Gly	Thr	Glu	Pro	Ser 300
Asp	Ile	Ile	Ile	Pro 305	Leu	Arg	Thr	Thr	Glu 310	Asn	Asn	Tyr	Cys	Pro 315
His	Tyr	Glu	Lys	Val 320	Ser	Gly	Asp	Tyr	Gly 325	His	Pro	Val	Tyr	Ile 330
Val	Gln	Glu	Met	Pro 335	Pro	Gln	Ser	Pro	Ala 340	Asn	Ile	Tyr	Tyr	Lys 345
Val 346														



(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
- Met Ala Val Arg Arg Asp Ser Val Trp Lys Tyr Cys Trp Gly Val 1 5 10
- Leu Met Val Leu Cys Arg Thr Ala Ile Ser Lys Ser Ile Val Leu
 20 25 30
- Glu Pro Ile Tyr Trp Asn Ser Ser Asn Ser Lys Phe Leu Pro Gly
 35 40 45
- Gln Gly Leu Val Leu Tyr Pro Gln Ile Gly Asp Lys Leu Asp Ile
 50 55 60
- Ile Cys Pro Lys Val Asp Ser Lys Thr Val Gly Gln Tyr Glu Tyr
 65 70 75
- Tyr Lys Val Tyr Met Val Asp Lys Asp Gln Ala Asp Arg Cys Thr 80 85 90
- Ile Lys Lys Glu Asn Thr Pro Leu Leu Asn Cys Ala Lys Pro Asp 95 100 105
- Gln Asp Ile Lys Phe Thr Ile Lys Phe Gln Glu Phe Ser Pro Asn 110 115 120
- Leu Trp Gly Leu Glu Phe Gln Lys Asn Lys Asp Tyr Tyr Ile Ile 125 130 135
- Ser Thr Ser Asn Gly Ser Leu Glu Gly Leu Asp Asn Gln Glu Gly
 140 145 150
- Gly Val Cys Gln Thr Arg Ala Met Lys Ile Leu Met Lys Val Gly
 155 160 165
- Gln Asp Ala Ser Ser Ala Gly Ser Thr Arg Asn Lys Asp Pro Thr 170 175 180
- Arg Arg Pro Glu Leu Glu Ala Gly Thr Asn Gly Arg Ser Ser Thr
 185 190 195

84

P

Thr	Ser	Pro	Phe	Val 200	Lys	Pro	Asn	Pro	Gly 205	Ser	Ser	Thr	Asp	Gly 210
Asn	Ser	Ala	Gly	His 215	Ser	Gly	Asn	Asn	Ile 220	Leu	Gly	Ser	Glu	Val 225
Ala	Leu	Phe	Ala	Gly 230	Ile	Ala	Ser	Gly	Cys 235	Ile	Ile	Phe	Ile	Val 240
Ile	Ile	Ile	Thr	Leu 245	Val	Val	Leu	Leu	Leu 250	Lys	Tyr	Arg	Arg	Arg 255
His	Arg	Lys	His	Ser 260	Pro	Gln	His	Thr	Thr 265	Thr	Leu	Ser	Leu	Ser 270
Thr	Leu	Ala	Thr	Pro 275	Lys	Arg	Ser	Gly	Asn 280	Asn	Asn	Gly	Ser	Glu 285
Pro	Ser	Asp	Ile	Ile 290	Ile	Pro	Leu	Arg	Thr 295	Ala	Asp	Ser	Val	Phe 300
Cys	Pro	His	Tyr	Glu 305	Lys	Val	Ser	Gly	Asp 310	Tyr	Gly	His	Pro	Val 315
Tyr	Ile	Val	Gln	Glu 320	Met	Pro	Pro	Gln	Ser 325	Pro	Ala	Asn	Ile	Tyr 330
Tyr	Lys	Val 333												

